REMARKS

Claims 1, 2-4, 10-11 and 23 remain in the application. Only Claims 1, 12 and 23 are in independent form. Reconsideration of the subject application as amended pursuant to and consistent with 37 C.F.R. §1.112 and in light of the remarks which follow are respectfully requested.

With the present response Applicants have corrected typographical errors found in the specification. Applicants enclose a set of modified pages of the description for the benefit of the Examiner.

Applicants have also corrected obvious errors found in the specification. A marked-up version of the changes made to the specification are found in the "Version with markings to show changes made" attached to this paper. The following clarifications are provided for the Examiner's benefit:

a) The error contained at page 4 line 24.

Point N°14 was referring to itself. This point thus obviously contains an error. Point 14 refers to a recombinant polypeptide. Point N°13 page 4 line 21 refers to a purified or isolated recombinant polypeptide comprising the amino acid sequence of secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide. By reading the specification it is obvious that point N°14 should refer to point N°13.

b) The error contained at page 20 line 26.

Page 20 line 26 relates to a polypeptide comprising an amino acid sequence having particular percentage of identity with cited amino acid sequences under which are SEQ ID N°4-6, SEQ ID N°10-12, SEQ ID N°16-17. However it refers to SEQ ID N°19 which is a DNA sequence corresponding to full length $\alpha_2\delta$-2. This paragraph thus obviously contains an error. By reading the specification it is obvious that this paragraph should refer to SEQ ID N°18. This obvious correction is further demonstrated by the reading of page 20 line 34 of the specification which mentions SEQ ID N°4-6, SEQ ID N°10-12 and SEQ ID N°16-18 as being preferred amino acids sequences of the invention.

c) The error contained at page 31 line 20 and 25.

Example 11 relates to a nucleotide sequence encoding a soluble secreted mouse $\alpha_2\delta$-3 deletion mutant of cited amino acid sequence. However it refers to SEQ ID N°25 which is a DNA sequence. This example thus obviously contains an error. By reading the specification it is obvious that this paragraph should refer to SEQ ID N°24. This obvious correction is further demonstrated by the reading of page 33 line 9-10.

In the following paragraph, Applicants first provide a summary of some of the key points of the present invention. This is followed by comments to the specific rejections set forth in the Office Action.

The invention relates to truncated $\alpha_2\delta$ calcium channel subunit cDNA sequences which encode soluble secreted polypeptides which lack a C-terminal portion of the corresponding native protein while retaining their calcium channel subunit properties.

The term "soluble secreted $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit" is intended to designate polypeptide sequences which, when produced by a recombinant host cell, are secreted at least partially into the culture medium rather than remaining associated with the host cell membrane (see the specification at page 8 lines 5-9).

Full length $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunits are membrane associated and thus <u>are not secreted soluble</u>. Therefore full length $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunits are not part of the invention.

Preferably the secreted soluble $\alpha_2\delta$ calcium channel subunit are human $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 polypeptides. However, due to cross species homology for the $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit, the C-terminal deletion may also be applied to other eukaryotic species.

The present application specifically discloses the following deletion mutants:

For human $\alpha_2\delta$-2:

- a 1062 amino acid long mutant (see nucleic sequence SEQ ID N°1 and amino acid sequence SEQ ID N°4)
- a 1082 amino acid long mutant (see nucleic sequence SEQ ID N°2 and amino acid sequence SEQ ID N°5)
- a 1109 amino acid long mutant (see nucleic sequence SEQ ID N°3 and amino acid sequence SEQ ID N°6).

For human $\alpha_2\delta$-3:
- a 1019 amino acid long mutant (see nucleic sequence SEQ ID N°7 and amino acid sequence SEQ ID N°10)
- a 1038 amino acid long mutant (see nucleic sequence SEQ ID N°8 and amino acid sequence SEQ ID N°11)
- a 1065 amino acid long mutant (see nucleic sequence SEQ ID N°9 and amino acid sequence SEQ ID N°12).

For human $\alpha_2\delta$-4:
- a 304 amino acid long mutant (see nucleic sequence SEQ ID N°13 and amino acid sequence SEQ ID N°16)
- a 323 amino acid long mutant (see nucleic sequence SEQ ID N°14 and amino acid sequence SEQ ID N°17)
- a 350 amino acid long mutant (see nucleic sequence SEQ ID N°15 and amino acid sequence SEQ ID N°18).

The use of some of these mutants is further illustrated through the examples referring to SEQ ID N°23 which is a truncated $\alpha_2\delta$-2 which corresponds to a 1109 amino acid long mutant to which a 6His tag has been added and the example relating to SEQ ID N°24 which is a $\alpha_2\delta$-3 deletion mutant to which a 6His tag has been added.

Claims 1, 9 and 12 stand rejected under 35 U.S.C §112, first paragraph, because the specification, while enabling for nucleotides encoding SEQ ID NO: 20 and 22, does not reasonably provide enablement for a nucleic acid encoding any other polypeptide.

The objection against Claim 9 can now be withdrawn since this claim has been deleted.

With regard to Claims 1 and 12, Applicants respectfully submit that these claims refer to secreted soluble polypeptides of $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 subunit. It is to be noted that SEQ ID NO: 20 and SEQ ID NO: 22 refer to full length sequences and do not fall into the scope of Claim 1.

Truncated $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 subunits have been illustrated by 3 specific sequences respectively. The one skilled in the art has enough guidance to create other deletion mutants which are secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptides which retain their voltage-dependent calcium channel properties. Experimentation will be necessary to determine the interest of using shorter or longer mutants but the skilled person has an expectation of success based on the initial guidance of the specification and hence no undue experimentation is necessary.

In view of the above, withdrawal of the rejection of Claims 1, 9 and 12 under 35 USC §112, first paragraph is respectfully requested.

Claims 2-3 and 5 stand rejected under 35 U.S.C §112, first paragraph, because the specification while being enabling for a polynucleotide encoding a substantially purified polypeptide comprising an amino acid sequence set forth in SEQ ID NO: 20 and 22, does not reasonably provide enablement for a polynucleotide encoding a substantially purified variant having at least 90% amino acids sequence identity to SEQ ID NO 20 and 22. The specification does not enable any person skilled in the art to which it pertains or with which it is most nearly connected to make and use the invention commensurate in scope with these claims.

The objection against Claim 5 can now be withdrawn since this claim has been deleted.

In response, Applicants wish to point out that Claims 2 and 3 have been amended to clarify the types of amino acids substitutions which can be contemplated by the skilled person.

Amended Claim 2 is supported by the specification at page 20, line 36 to the end of page 21.

Amended Claim 3 is supported by the specification at page 20, line 36 to the end of page 21.

In view of amended Claims 2 and 3, withdrawal of the rejection of those claims under 35 USC §112, first paragraph is respectfully requested.

Claims 1, 7, 9 and 12 stand rejected under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regards as the invention.

The Examiner indicates that Claims 1, 9 and 12 are indefinite in that they only describe the peptide of interest by an arbitrary protein name, i.e., "alpha2delta-2" and that nothing in the claims distinctly identifies the protein.

The objection against Claim 9 can now be withdrawn since this claim has been deleted.

In response, Applicants wish to point out that protein names $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 are definite, per se, for one of ordinary skill in the art. As an example, Klugbauer et al. (The Journal of Neuroscience, January 15, 1999, 19(2): 684-691) describe two forms of the full length calcium channel $\alpha_2\delta$-2 subunit and one form of the full length calcium channel $\alpha_2\delta$-3 subunit. Thus, the wording $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 provide adequate guidance as to the nature of the polypeptide which Applicants claim.

Furthermore, Applicants wish to point out that the $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 subunit polypeptides of the invention are defined as mammalian secreted soluble cerebral cortical voltage-dependent calcium channel subunit polypeptides. Thus Claims 1, 9 and 12 distinctly claim the subject matter of the invention.

In view of the above, withdrawal of the rejection of Claims 1, 9 and 12 under 35 USC §112, second paragraph, is respectfully requested.

The Examiner also indicates that Claims 7 and 9 are indefinite because they recite the term "stringent conditions" which is a conditional term and because some nucleic acids which might hybridize under conditions of moderate stringency for example would fail to hybridize under conditions of high stringency.

The objection against Claims 7 and 9 can now be withdrawn since these claims have been deleted.

Claims 1, 4 and 10-12 stand rejected under 35 USC §102(b). The Examiner explains that Wei et al. disclose a human α_2 calcium channel which is 100% identical to SEQ ID NO: 1.

In response Applicants provide herewith as Exhibit 1 a sequence alignment of the human α2 calcium channel sequence disclosed in Wei et al. and SEQ ID NO: 1 disclosed in the present application.

This alignment shows that Wei et al. disclose a full length human $\alpha_2\delta$-2 subunit polypeptide (5463 nucleotides (AF042792)) whereas SEQ ID NO: 1 of the present application is a truncated version of this full length polypeptide (3186 nucleotides). Thus the sequence of the α2 calcium channel disclosed by Wei et al. is not the same sequence as sequence SEQ ID NO: 1. Therefore, the α2 calcium channel disclosed by Wei et al. is not 100% identical to the sequence of SEQ ID NO: 1. Furthermore it is clear from this

analysis that Wei et al. does not disclose any form of truncated calcium channel subunit. Hence Claims 1, 4, 10-12 are novel over this prior art.

The amendment of Claim 4 results from a typographical error. Appropriate sequences to be incorporated in this claim are provided at page 10, lines 16-19 of the specification as filed.

In view of the arguments set forth above withdrawal of the rejection of Claims 1, 4 and 10-12 under 35 USC §102(b) is respectfully requested.

Claims 1, 6, 7 and 9-12 are rejected under 35 USC §102(b) as being anticipated by WO9504822.

The objection against Claims 6, 7 and 9 can now be withdrawn since those claims have been deleted.

The Examiner explains that Harpold et al. disclose the cloning and expression of human voltage gated calcium channel subunits thus anticipating Claim 1.

In response, Applicants wish to draw the attention of the Examiner to the fact that Claim 1 refers to secreted soluble voltage-dependent calcium channel $\alpha_2\delta$-2, $\alpha_2\delta$-3, $\alpha_2\delta$-4 subunit polypeptides and not only to voltage gated Ca^{2+} subunits. Therefore, Harpold et al. do not disclose a purified or isolated nucleic acid encoding a mammalian secreted soluble cerebral cortical voltage-dependent calcium channel $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide of Claim 1.

In conclusion Claim 1 is not anticipated by Harpold et al.

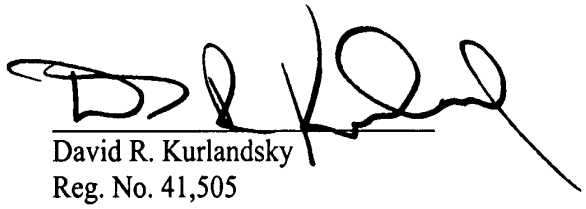
In view of the arguments set forth above withdrawal of the rejection of Claims 1, 6, 7 and 9 under 35 USC §102(b) is respectfully requested.

In view of the foregoing, further and favorable action in the form of a Notice of Allowance is believed to be next in order, and such action is earnestly solicited.

The Commissioner is hereby authorized to charge any fees under 37.C.F.R §1.116 and 1.117 that may be required by this paper to Deposit Account No. 23-0455.

In the event the Examiner wishes to discuss any matter concerning this application, he is invited to communicate with the undersigned.

Respectfully submitted,



David R. Kurlandsky
Reg. No. 41,505
Warner-Lambert Company
2800 Plymouth Road
Ann Arbor, MI 48105
Tel. (734) 622-7304
Fax (734) 622-1553

Attachment - Amendments to the specification and claims, Version with markings to show changes made
Exhibit 1

DK1P4407.doc

"Version with markings to show changes made."

IN THE SPECIFICATION:

Please correct the following typographical errors:

At page 2, second paragraph:

The only assay currently available for the screening of ligands that bind the $\alpha_2\delta$ subunit involves the use of pig membrane extracts as a source of the $\alpha_2\delta$ subunit. Such an assay presents major inconvenients. Firstly, [bcause] because the assay material is a membrane extract, it is very difficult to accurately determine the protein composition from one assay preparation to another particularly with regard to the subtype. Also, the presence of various impurities in the assay preparation is a problem in small plate assays. Furthermore, as the protein preparation lacks homogeneity, the interaction between the targeted protein and the assay plate is often quite uneven. This [rendres] renders the streamlining of the assay in a high throughput format almost impossible to achieve.

At page 4, sixth paragraph:

14) A recombinant polypeptide according to [14)] 13), having at least 80% amino-acid identity with a polypeptide comprising:

- from amino acid 1 to between amino acids 1027 and 1062 of the amino acid sequence of SEQ ID N°20, or
- from amino acid 1 to between amino acids 1019 and 1079 of the amino acid sequence of SEQ ID N°22.

At page 9, first paragraph:

their native folding and hence [thir] their [^{3}H]gabapentin binding properties are those corresponding to the native protein in which amino-acid stretch __984__ to __C-terminal end__ of the amino-acid sequence of SEQ ID N°22 has been deleted. The skilled scientist can quite easily determine within this amino-acid stretch the optimal $\alpha_2\delta$-3 subunit polypeptides.

At page 10, second full paragraph:

(a) a purified or isolated nucleic acid encoding [a] a secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit having at least 80% amino acid identity with the polypeptide of SEQ ID N°20 or 22, or a sequence complementary thereto;

At page 18, second paragraph:

Once the optimal radioligand binding conditions have been determined, a test ligand can be introduced in the assay medium to evaluate the level of displacement of the radioligand. The concentration of test ligand to be introduced in the assay medium usually varies from 0.1 nM to about 100 [uM] μM. A preferred test ligand concentration of about 10 [uM] μM is usually a starting point in a high throughput screening assay. Then, depending on the number of hits obtained, it may be lowered or increased.

At page 18, sixth paragraph:

The interaction of the secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide with the flashplates can be optimized by adjusting the concentration of the polypeptide and by introducing a reagent which will favor this interaction. When a standard NEN Ni chelate flashplate is used, the secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide volume usually varies between 0.5 and 20 [ul] μl for a concentration of secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide of 0.6 [pmol/ul] pmol/μl. As the published maximum binding capacity of

At page 19, first paragraph:

NEN p plates is about 6 pmol per well, the inventors consider that an optimal concentration of secreted $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide is probably around 5 pmol per well at 8 [ul] μl.

At page 19, second paragraph:

With regard to the reagent favoring the interaction between the secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide and the radioligand as well as the flashplates, the inventors believe that imidazole could also be efficiently used for that purpose when the secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide is tagged with an amino acid sequence including 6 histidine residues. The inventors also believe that imidazole concentrations can substantially [enhanced] enhance binding of the radioligand to the secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 polypeptide. The optimal concentration of imidazole used to enhance radioligand binding varies depending on the concentration of secreted soluble $\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 subunit polypeptide used in the assay. For instance, when the volume of the $\alpha_2\delta$-1 subunit polypeptide is about 10 [ul ul] µl ($\alpha_2\delta$-2, $\alpha_2\delta$-3 or $\alpha_2\delta$-4 polypeptide concentration of 0.6 [pmol/ul] pmol/µl), the optimal imidazole concentration can vary between 1 and 20 mM, with a concentration of about 10 mM being preferred. As mentioned previously, other compounds such as histidine as well as pH variations may be used to enhance radioligand binding.

At page 19, fourth paragraph:

Once the optimal radioligand binding conditions have been determined, a test ligand can be introduced in the assay medium to evaluate the level of displacement of the radioligand. The concentration of test ligand to be introduced in the assay medium usually varies from 0.1 nM to about 100 [uM] µM. A preferred test ligand concentration of about 10 [uM] µM is usually a

At page 20, fifth paragraph:

In a further preferred embodiment, the polypeptide comprises an amino acid sequence having at least 80%, preferably 90%, more preferably 95%, and most preferably 98% or 99% amino acid identity with the amino acid sequence of SEQ ID N°4, SEQ ID N°5, SEQ ID N°6, SEQ ID N°10, SEQ ID N°11, SEQ ID N°12, SEQ ID N°16, SEQ ID N°17 and [SEQ ID N°19] SEQ ID N°18.

At page 29, fourth paragraph:

Example 8

Ni Flashplate assay of [^{3}H]Leucine binding to secreted soluble human $\alpha_2\delta$-2-6His

The procedure described in example 7 is repeated, except that [^{3}H]gabapentin is replaced by 25 [ul] µl (10.1 nM) of [^{3}H]Leucine (41 Ci/mmole).

At page 30, first indentation under **Example 9**:

25µl 10 mM HEPES pH7.4 or 25 [ul othe] µl of the test compound at the appropriate concentration in HEPES

At page 31, third paragraph:

Example 11

Construction of a nucleotide sequence encoding a soluble secreted mouse $\alpha_2\delta$-3 deletion mutant of SEQ ID N°25 as follows.

a) Primer design

PCR primers were designed to generate the secreted soluble mouse $\alpha_2\delta$-3 deletion mutant of [SEQ ID N° 25] SEQ ID N°24 as follows:

IN THE CLAIMS:

Please amend Claims 2, 3 and 4 as follows:

Claim 2 (amended). A purified or isolated nucleic acid according to claim 1, comprising a polynucleotide having at least 90% identity with the sequence encoding :

- from amino-acid 1 to between amino-acids 1027 and 1062 of SEQ ID N°20 for $\alpha_2\delta$-2,
- from amino-acid 1 to between amino-acids 984 and 1019 of SEQ ID N°22 for $\alpha_2\delta$-3

wherein the differing nucleotides encode amino acids which are the same as the amino acids of the SEQ ID N°20 and SEQ ID N°22 through codon degeneracy or encode amino acids which are equivalent to the amino acids of SEQ ID N°20 and SEQ ID N°22 either by structural homology, by net charge or hydrophobicity similarity, such that the encoded polypeptide retains its specificity and affinity properties to the biological targets of the parent polypeptides.

Claim 3 (amended). A purified or isolated nucleic acid according to claim 1, having at least 90% identity with the sequence encoding :

- from amino-acid 1 to between amino-acids 1047 and 1062 of SEQ ID N°20 for $\alpha_2\delta$-2,
- from amino-acid 1 to between amino-acids 1004 and 1019 of SEQ ID N°22 for $\alpha_2\delta$-3

wherein the differing nucleotides encode amino acids which are the same as the amino acids of the SEQ ID N°20 and SEQ ID N°22 through codon degeneracy or encode amino acids which are equivalent to the amino acids of SEQ ID N°20 and SEQ ID N°22 either by structural homology, by net charge or hydrophobicity similarity, such that the encoded polypeptide retains its specificity and affinity properties to the biological targets of the parent polypeptides.

Claim 4 (amended). A purified or isolated nucleotide sequence according to claim 1 wherein said sequence is the sequence of SEQ ID N°1, SEQ ID N°2, SEQ ID N°3, SEQ ID N°7, SEQ ID N°8, SEQ ID N°9, SEQ ID N°13, SEQ ID N°14, or SEQ ID N°15[, SEQ ID N°19 or SEQ ID N°21].

Please delete Claims 5, 6, 7 and 9.

Please add new Claim 23.

Claim 23 (NEW). A purified or isolated nucleic acid having at least 90% identity with the nucleotide sequence of SEQ ID N°1, SEQ ID N°2, SEQ ID N°3, SEQ ID N°7, SEQ ID N°8, SEQ ID N°9, SEQ ID N°13, SEQ ID N°14, or SEQ ID N°15.

Exhibit 1

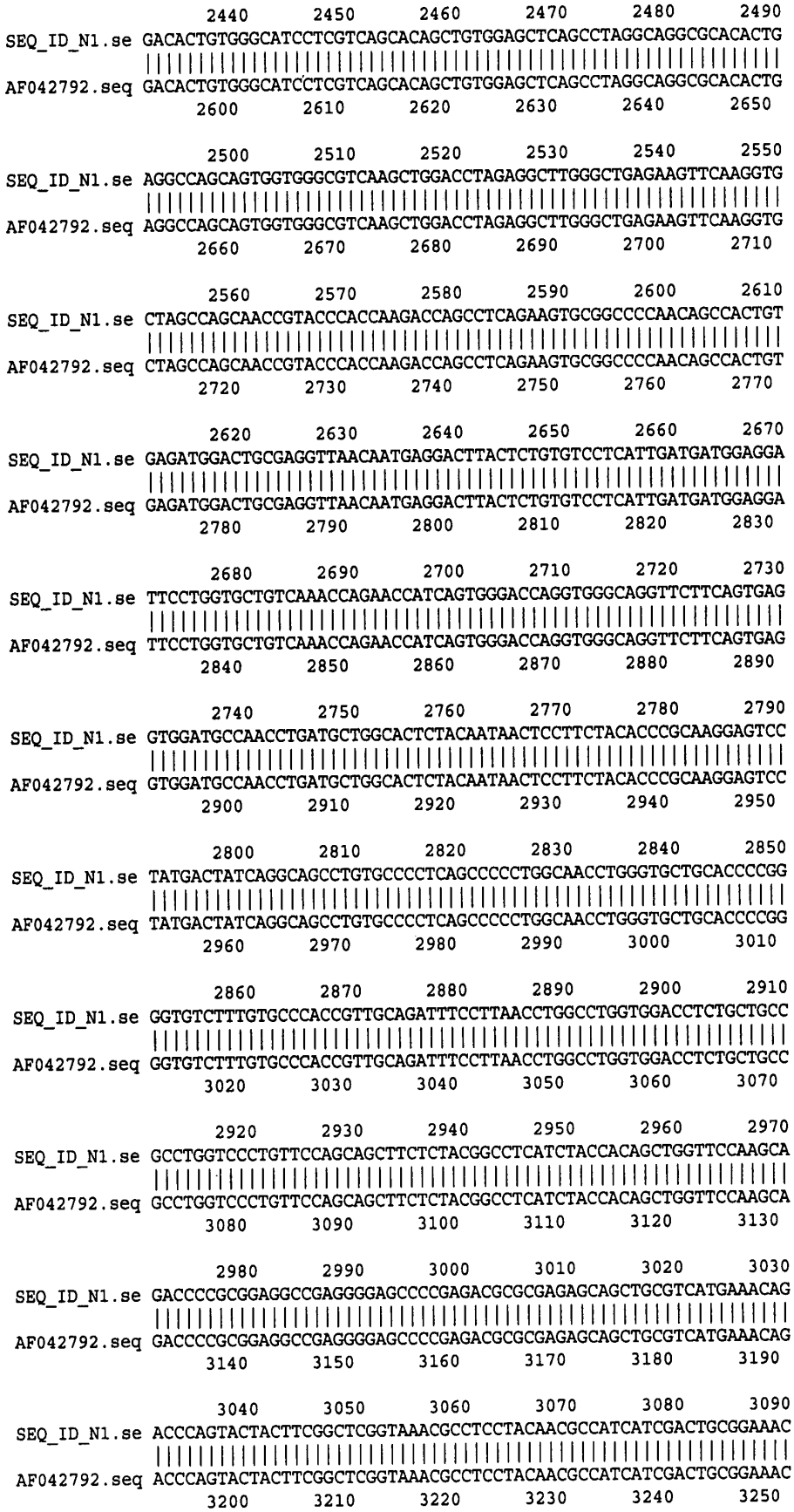
Sequence alignement of sequence SEQ ID N°1 of the patent application and the sequence of the human alpha 2 calcium channel disclosed by Wei et al. (AF042792)

```
SEQ_ID_N1.se

AF042792.seq                                                        GCCAGCGCTGC
                                                                            10

SEQ_ID_N1.se

AF042792.seq AGGGAGATAGCAGCGCGCAGCCCGCAGAGGCGCTGCGGCCCGTGCAGCCCCGGAGGCCCC
                    20        30        40        50        60        70

SEQ_ID_N1.se

AF042792.seq TCGCGGAGAAGGCGGCGGCGGAGGAGAGGCCGAGTTACCGCCCGCCGCCCGCGCCCCCCC
                    80        90       100       110       120       130

                                                  10        20        30
SEQ_ID_N1.se                                      ATGGCGGTGCCGGCTCGGACCTGCGGCGCC
                                                  ||||||||||||||||||||||||||||||
AF042792.seq TCCCCGCGGCGCCGCATCTTGAATGGAAACATGGCGGTGCCGGCTCGGACCTGCGGCGCC
                   140       150       160       170       180       190

                     40        50        60        70        80        90
SEQ_ID_N1.se TCTCGGCCCGGCCCAGCGCGGACTGCGCGCCCCTGGCCCGGCTGCGGCCCCCACCCTGGC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TCTCGGCCCGGCCCAGCGCGGACTGCGCGCCCCTGGCCCGGCTGCGGCCCCCACCCTGGC
                   200       210       220       230       240       250

                    100       110       120       130       140       150
SEQ_ID_N1.se CCCGGCACCCGGCGCCCGACGTCCGGGCCCCCGCGCCCGCTGTGGCTGCTGCTGCCGCTT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CCCGGCACCCGGCGCCCGACGTCCGGGCCCCCGCGCCCGCTGTGGCTGCTGCTGCCGCTT
                   260       270       280       290       300       310

                    160       170       180       190       200       210
SEQ_ID_N1.se CTACCGCTGCTCGCCGCCCCCGGCGCCTCTGCCTACAGCTTCCCCCAGCAGCACACGATG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CTACCGCTGCTCGCCGCCCCCGGCGCCTCTGCCTACAGCTTCCCCCAGCAGCACACGATG
                   320       330       340       350       360       370

                    220       230       240       250       260       270
SEQ_ID_N1.se CAGCACTGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CAGCACTGGGCCCGGCGTCTGGAGCAGGAGGTCGACGGCGTGATGCGGATTTTTGGAGGC
                   380       390       400       410       420       430

                    280       290       300       310       320       330
SEQ_ID_N1.se GTCCAGCAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAAT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GTCCAGCAGCTCCGTGAGATTTACAAGGACAACCGGAACCTGTTCGAGGTACAGGAGAAT
                   440       450       460       470       480       490

                    340       350       360       370       380       390
SEQ_ID_N1.se GAGCCTCAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GAGCCTCAGAAGTTGGTGGAGAAGGTGGCAGGGGACATTGAGAGCCTTCTGGACAGGAAG
                   500       510       520       530       540       550

                    400       410       420       430       440       450
SEQ_ID_N1.se GTGCAGGCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GTGCAGGCCCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAAGCACACCGCTGG
```

```
                    560       570       580       590       600       610

                   460       470       480       490       500       510
SEQ_ID_N1.se CAGGACAACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CAGGACAACATCAAGGAGGAAGACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTG
                   620       630       640       650       660       670

                   520       530       540       550       560       570
SEQ_ID_N1.se GACGACCCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGAC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GACGACCCTGAGAGTGAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCTAAGGCTGGAC
                   680       690       700       710       720       730

                   580       590       600       610       620       630
SEQ_ID_N1.se TTCATCGAGGACCCAAACTTCAAGAACAAGGTCAACTATTCATACGCGGCTGTACAGATC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TTCATCGAGGACCCAAACTTCAAGAACAAGGTCAACTATTCATACGCGGCTGTACAGATC
                   740       750       760       770       780       790

                   640       650       660       670       680       690
SEQ_ID_N1.se CCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAGGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CCTACGGACATCTACAAAGGCTCCACTGTCATCCTCAATGAGCTCAACTGGACAGAGGCC
                   800       810       820       830       840       850

                   700       710       720       730       740       750
SEQ_ID_N1.se CTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCCACACTGCTGTGGCAGGTCTTC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CTGGAGAATGTGTTCATGGAAAACCGCAGACAAGACCCCACACTGCTGTGGCAGGTCTTC
                   860       870       880       890       900       910

                   760       770       780       790       800       810
SEQ_ID_N1.se GGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAGAAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCCGTGGCGAGCCCCCAAGAAG
                   920       930       940       950       960       970

                   820       830       840       850       860       870
SEQ_ID_N1.se ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCACCCAAA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq ATCGACCTGTACGATGTCCGAAGGAGACCCTGGTATATCCAGGGGGCCTCGTCACCCAAA
                   980       990      1000      1010      1020      1030

                   880       890       900       910       920       930
SEQ_ID_N1.se GACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAGCTGATG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GACATGGTCATCATCGTGGATGTGAGTGGCAGTGTGAGCGGCCTGACCCTGAAGCTGATG
                  1040      1050      1060      1070      1080      1090

                   940       950       960       970       980       990
SEQ_ID_N1.se AAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAATGTGGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq AAGACATCTGTCTGCGAGATGCTGGACACGCTGTCTGATGATGACTATGTGAATGTGGCC
                  1100      1110      1120      1130      1140      1150

                  1000      1010      1020      1030      1040      1050
SEQ_ID_N1.se TCGTTCAACGAGAAGGCACAGCCTGTGTCATGCTTCACACACCTGGTGCAGGCCAATGTG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TCGTTCAACGAGAAGGCACAGCCTGTGTCATGCTTCACACACCTGGTGCAGGCCAATGTG
                  1160      1170      1180      1190      1200      1210

                  1060      1070      1080      1090      1100      1110
SEQ_ID_N1.se CGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAGGGCACCACAGGC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAGGGCACCACAGGC
                  1220      1230      1240      1250      1260      1270
```

```
                    1120       1130       1140       1150       1160       1170
SEQ_ID_N1.se TACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAACATCACTCGGGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TACAAGGCCGGCTTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAACATCACTCGGGCC
                    1280       1290       1300       1310       1320       1330

                    1180       1190       1200       1210       1220       1230
SEQ_ID_N1.se AACTGCAACAAGATGATCATGATGTTCACGGATGGTGGTGAGGACCGCGTGCAGGACGTC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq AACTGCAACAAGATGATCATGATGTTCACGGATGGTGGTGAGGACCGCGTGCAGGACGTC
                    1340       1350       1360       1370       1380       1390

                    1240       1250       1260       1270       1280       1290
SEQ_ID_N1.se TTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTTTACTTTCTCCGTGGGGCAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TTTGAGAAGTACAATTGGCCAAACCGGACGGTGCGCGTGTTTACTTTCTCCGTGGGGCAG
                    1400       1410       1420       1430       1440       1450

                    1300       1310       1320       1330       1340       1350
SEQ_ID_N1.se CATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCCAACAAAGGCTACTATTTT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CATAACTATGACGTCACACCGCTGCAGTGGATGGCCTGTGCCAACAAAGGCTACTATTTT
                    1460       1470       1480       1490       1500       1510

                    1360       1370       1380       1390       1400       1410
SEQ_ID_N1.se GAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAATATCTAGATGTGTTGGGC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GAGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAATATCTAGATGTGTTGGGC
                    1520       1530       1540       1550       1560       1570

                    1420       1430       1440       1450       1460       1470
SEQ_ID_N1.se AGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAGTGGACCAACGTGTATGAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq AGGCCCATGGTGCTGGCAGGCAAGGAGGCCAAGCAGGTTCAGTGGACCAACGTGTATGAG
                    1580       1590       1600       1610       1620       1630

                    1480       1490       1500       1510       1520       1530
SEQ_ID_N1.se GATGCACTGGGACTGGGGTTGGTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GATGCACTGGGACTGGGGTTGGTGGTAACAGGGACCCTCCCTGTTTTCAACCTGACACAG
                    1640       1650       1660       1670       1680       1690

                    1540       1550       1560       1570       1580       1590
SEQ_ID_N1.se GATGGCCCTGGGGAAAAGAAGAACCAGCTGATCCTGGGCGTGATGGGCATTGACGTGGCT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GATGGCCCTGGGGAAAAGAAGAACCAGCTGATCCTGGGCGTGATGGGCATTGACGTGGCT
                    1700       1710       1720       1730       1740       1750

                    1600       1610       1620       1630       1640       1650
SEQ_ID_N1.se CTGAATGACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CTGAATGACATCAAGAGGCTGACCCCCAACTACACGCTTGGAGCCAACGGCTATGTGTTT
                    1760       1770       1780       1790       1800       1810

                    1660       1670       1680       1690       1700       1710
SEQ_ID_N1.se GCCATTGACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAAC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GCCATTGACCTGAACGGCTACGTGTTGCTGCACCCCAATCTCAAGCCCCAGACCACCAAC
                    1820       1830       1840       1850       1860       1870

                    1720       1730       1740       1750       1760       1770
SEQ_ID_N1.se TTCCGGGAGCCTGTGACTCTGGACTTCCTGGATGCGGAGCTAGAGGATGAGAACAAGGAA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TTCCGGGAGCCTGTGACTCTGGACTTCCTGGATGCGGAGCTAGAGGATGAGAACAAGGAA
                    1880       1890       1900       1910       1920       1930
```

```
                1780       1790       1800       1810       1820       1830
SEQ_ID_N1.se GAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCACAAGCAGATCAGAACGTTGGTC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GAGATCCGTCGGAGCATGATTGATGGCAACAAGGGCCACAAGCAGATCAGAACGTTGGTC
                1940       1950       1960       1970       1980       1990

                1840       1850       1860       1870       1880       1890
SEQ_ID_N1.se AAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGGAACTACACCTGGGTGCCTATA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq AAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGGAACTACACCTGGGTGCCTATA
                2000       2010       2020       2030       2040       2050

                1900       1910       1920       1930       1940       1950
SEQ_ID_N1.se AGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCCTACAGCACCTTCTACCTCCAA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq AGGAGCACTAACTACAGCCTGGGGCTGGTGCTCCCACCCTACAGCACCTTCTACCTCCAA
                2060       2070       2080       2090       2100       2110

                1960       1970       1980       1990       2000       2010
SEQ_ID_N1.se GCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTTGAGTTCCTGCTCCCCAGCAGC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTTGAGTTCCTGCTCCCCAGCAGC
                2120       2130       2140       2150       2160       2170

                2020       2030       2040       2050       2060       2070
SEQ_ID_N1.se TTTGAGTCTGAAGGACACGTTTTCATTGCTCCCAGAGAGTACTGCAAGGACCTGAATGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TTTGAGTCTGAAGGACACGTTTTCATTGCTCCCAGAGAGTACTGCAAGGACCTGAATGCC
                2180       2190       2200       2210       2220       2230

                2080       2090       2100       2110       2120       2130
SEQ_ID_N1.se TCAGACAACAACACCGAGTTCCTGAAAAACTTTATTGAGCTCATGGAGAAAGTGACTCCA
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TCAGACAACAACACCGAGTTCCTGAAAAACTTTATTGAGCTCATGGAGAAAGTGACTCCA
                2240       2250       2260       2270       2280       2290

                2140       2150       2160       2170       2180       2190
SEQ_ID_N1.se GACTCCAAGCAGTGCAACAACTTCCTTCTGCACAACCTGATCTTGGACACGGGCATCACG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GACTCCAAGCAGTGCAACAACTTCCTTCTGCACAACCTGATCTTGGACACGGGCATCACG
                2300       2310       2320       2330       2340       2350

                2200       2210       2220       2230       2240       2250
SEQ_ID_N1.se CAGCAGCTGGTAGAGCGTGTGTGGAGGGACCAGGATCTCAACACGTACAGCCTACTGGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq CAGCAGCTGGTAGAGCGTGTGTGGAGGGACCAGGATCTCAACACGTACAGCCTACTGGCC
                2360       2370       2380       2390       2400       2410

                2260       2270       2280       2290       2300       2310
SEQ_ID_N1.se GTGTTCGCTGCCACAGACGGTGGCATCACCCGAGTCTTCCCCAACAAGGCAGCTGAGGAC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GTGTTCGCTGCCACAGACGGTGGCATCACCCGAGTCTTCCCCAACAAGGCAGCTGAGGAC
                2420       2430       2440       2450       2460       2470

                2320       2330       2340       2350       2360       2370
SEQ_ID_N1.se TGGACAGAGAACCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGCAGCCTGGATAACCAC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TGGACAGAGAACCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGCAGCCTGGATAACCAC
                2480       2490       2500       2510       2520       2530

                2380       2390       2400       2410       2420       2430
SEQ_ID_N1.se GGTTATGTCTTCAAGCCCCCACACCAGGATGCCCTGTTAAGGCCGCTGGAGCTGGAGAAT
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq GGTTATGTCTTCAAGCCCCCACACCAGGATGCCCTGTTAAGGCCGCTGGAGCTGGAGAAT
                2540       2550       2560       2570       2580       2590
```


2440 2450 2460 2470 2480 2490
SEQ_ID_N1.se GACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGCACACTG
AF042792.seq GACACTGTGGGCATCCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGCAGGCGCACACTG
2600 2610 2620 2630 2640 2650
2500 2510 2520 2530 2540 2550
SEQ_ID_N1.se AGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTCAAGGTG
AF042792.seq AGGCCAGCAGTGGTGGGCGTCAAGCTGGACCTAGAGGCTTGGGCTGAGAAGTTCAAGGTG
2660 2670 2680 2690 2700 2710
2560 2570 2580 2590 2600 2610
SEQ_ID_N1.se CTAGCCAGCAACCGTACCCACCAAGACCAGCCTCAGAAGTGCGGCCCCAACAGCCACTGT
AF042792.seq CTAGCCAGCAACCGTACCCACCAAGACCAGCCTCAGAAGTGCGGCCCCAACAGCCACTGT
2720 2730 2740 2750 2760 2770
2620 2630 2640 2650 2660 2670
SEQ_ID_N1.se GAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATTGATGATGGAGGA
AF042792.seq GAGATGGACTGCGAGGTTAACAATGAGGACTTACTCTGTGTCCTCATTGATGATGGAGGA
2780 2790 2800 2810 2820 2830
2680 2690 2700 2710 2720 2730
SEQ_ID_N1.se TTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGGTTCTTCAGTGAG
AF042792.seq TTCCTGGTGCTGTCAAACCAGAACCATCAGTGGGACCAGGTGGGCAGGTTCTTCAGTGAG
2840 2850 2860 2870 2880 2890
2740 2750 2760 2770 2780 2790
SEQ_ID_N1.se GTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACCCGCAAGGAGTCC
AF042792.seq GTGGATGCCAACCTGATGCTGGCACTCTACAATAACTCCTTCTACACCCGCAAGGAGTCC
2900 2910 2920 2930 2940 2950
2800 2810 2820 2830 2840 2850
SEQ_ID_N1.se TATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGTGCTGCACCCCGG
AF042792.seq TATGACTATCAGGCAGCCTGTGCCCCTCAGCCCCCTGGCAACCTGGGTGCTGCACCCCGG
2960 2970 2980 2990 3000 3010
2860 2870 2880 2890 2900 2910
SEQ_ID_N1.se GGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGGACCTCTGCTGCC
AF042792.seq GGTGTCTTTGTGCCCACCGTTGCAGATTTCCTTAACCTGGCCTGGTGGACCTCTGCTGCC
3020 3030 3040 3050 3060 3070
2920 2930 2940 2950 2960 2970
SEQ_ID_N1.se GCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTCATCTACCACAGCTGGTTCCAAGCA
AF042792.seq GCCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTCATCTACCACAGCTGGTTCCAAGCA
3080 3090 3100 3110 3120 3130
2980 2990 3000 3010 3020 3030
SEQ_ID_N1.se GACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAGAGCAGCTGCGTCATGAAACAG
AF042792.seq GACCCCGCGGAGGCCGAGGGGAGCCCCGAGACGCGCGAGAGCAGCTGCGTCATGAAACAG
3140 3150 3160 3170 3180 3190
3040 3050 3060 3070 3080 3090
SEQ_ID_N1.se ACCCAGTACTACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAAC
AF042792.seq ACCCAGTACTACTTCGGCTCGGTAAACGCCTCCTACAACGCCATCATCGACTGCGGAAAC
3200 3210 3220 3230 3240 3250

```
                    3100       3110       3120       3130       3140       3150
SEQ_ID_N1.se TGCTCCAGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCC
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AF042792.seq TGCTCCAGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGTGGTGGCC
                   3260       3270       3280       3290       3300       3310

                    3160       3170       3180
SEQ_ID_N1.se GAGAAGCCGCTGTGCAGCCAGTGCGAGGCTGGCCGG
             ||||||||||||||||||||||||||||||||||
AF042792.seq GAGAAGCCGCTGTGCAGCCAGTGCGAGGCTGGCCGGCTGCTGCAGAAGGAGACGCACTGC
                   3320       3330       3340       3350       3360       3370

SEQ_ID_N1.se

AF042792.seq CCAGCGGACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCGCGATACCGGAGAGGCCCG
                   3380       3390       3400       3410       3420       3430

SEQ_ID_N1.se

AF042792.seq             CACATCTGCTTCGACTACAACGCGACAGAAGATACCTCAGACTGTGGCC
                              3440       3450       3460       3470       3480

SEQ_ID_N1.se

AF042792.seq GCGGGGCCTCCTTCCCGCCGTCGCTGGGCGTCCTGGTCTCCCTGCAACTGCTGCTCCTCC
                   3490       3500       3510       3520       3530       3540

SEQ_ID_N1.se

AF042792.seq TGGGCCTGCCGCCCCGGCCGCAGCCTCAAGTCCTCGTCCACGCCTCTCGCCGCCTCTGAG
                   3550       3560       3570       3580       3590       3600

SEQ_ID_N1.se

AF042792.seq CACCCTGCCCCACCCCACCTCCACTCCCACCTCACCCGGCCTCTTCGCCTTTCCCACCCT
                   3610       3620       3630       3640       3650       3660

SEQ_ID_N1.se

AF042792.seq CCTGCCCCACACTCCCCGCCTTAGAGCCTCGTCCCTCCCTCACTGAAGGACCTGAGCTGG
                   3670       3680       3690       3700       3710       3720

SEQ_ID_N1.se

AF042792.seq CCAGGCCCTGAGAGTCTGGTCTGCGCCTTGGGATGGGGAGTCCCAAAGCGGGACGCCGCA
                   3730       3740       3750       3760       3770       3780

SEQ_ID_N1.se

AF042792.seq GGTGTTTGGCACCCAAATCACATCTCACCTCCGAACTGTTCAAGTGTCCCCAGACCCTTC
                   3790       3800       3810       3820       3830       3840

SEQ_ID_N1.se

AF042792.seq TTGCCTGCTGGGCTCCCCCCAGTGGGATGGGACAGGGAGGCCACACGCACTGGTGCCAAA
                   3850       3860       3870       3880       3890       3900

SEQ_ID_N1.se

AF042792.seq ACCAGGCCTCTGCTGCCGCCCTTCCTGGAGGCTGCCTATGTTGGGGGGGACCCTGCCTCA
                   3910       3920       3930       3940       3950       3960

SEQ_ID_N1.se

AF042792.seq GCTGACCCGGCCTCTCTGCCCCACCCAAGCCCAAACTTGGTTTCTGTGAGAATAGTGGAG
```

```
                    3970       3980       3990       4000       4010       4020

SEQ_ID_N1.se

AF042792.seq GAAGGTGAGATGGCCAGTTTGAAGCCTGTGCCTCCCAGCTTAAATCCTAGCAGGAGAGAG
                    4030       4040       4050       4060       4070       4080

SEQ_ID_N1.se

AF042792.seq GCTCTGGGGCAGCCCCCATGGGCTCCTGCCCCTTTCAGGCCTACAGCCACATCCCCAAGC
                    4090       4100       4110       4120       4130       4140

SEQ_ID_N1.se

AF042792.seq CCACCAGGTGTCAGGATAGTCACAGTGATACCAGTTCAGACACTACCCCATATACACCTG
                    4150       4160       4170       4180       4190       4200

SEQ_ID_N1.se

AF042792.seq GAACATTGAGGATGGAAACTGGACTCACATTCGACATACCCCACTGGGCACACGCACAAA
                    4210       4220       4230       4240       4250       4260

SEQ_ID_N1.se

AF042792.seq CACACACACTATGGGGTGGGGTGGGTGTAGGGGCTTACAAAGCCTTACACAGGGCGAGGG
                    4270       4280       4290       4300       4310       4320

SEQ_ID_N1.se

AF042792.seq GTTGGTGGGAGGGTTGGCACCTGCACACTCCATCTCCTGCTCACCACCTGCCTCTAATCT
                    4330       4340       4350       4360       4370       4380

SEQ_ID_N1.se

AF042792.seq GAGCTGCAGCCTGGCTGGTCCTCCCATTTCTAAAGCTGAATGTCAAACAGTGCCAAATGC
                    4390       4400       4410       4420       4430       4440

SEQ_ID_N1.se

AF042792.seq TGGGGCAGGGGGTGAAGAACCCTCTGTCCCACCCCTAGCCACCAGTGTCCTCCAAGTGCC
                    4450       4460       4470       4480       4490       4500

SEQ_ID_N1.se

AF042792.seq CCCTCACCTCTCCAGGTGCTCATTGTAACCATTTCTCACTAGTGTCAGGCCCCCAGTGGG
                    4510       4520       4530       4540       4550       4560

SEQ_ID_N1.se

AF042792.seq ACCACATGCCACTGCCTGCACCTTTCGGCAGAGGAACCCCCACCAGACATCACCCTTTGC
                    4570       4580       4590       4600       4610       4620

SEQ_ID_N1.se

AF042792.seq CTTAGCAGGGGTGACTTTGTCTCTCCTGGCTGGGCCATCCTTCCGCCAATCTGGCCCTTA
                    4630       4640       4650       4660       4670       4680

SEQ_ID_N1.se

AF042792.seq CACACTCAGGCCTGTGCCCACTCCCTATCTCCTTCCCACCCCTACACACACACTCCCTGC
                    4690       4700       4710       4720       4730       4740

SEQ_ID_N1.se

AF042792.seq TTGCAGGAGGCCAAACTGTCCCTCCCTTGCTGAACACACACACACACACACACACACAGG
                    4750       4760       4770       4780       4790       4800
```

SEQ_ID_N1.se

AF042792.seq TGGGGACTGGGCACAGCTCTTCACACCATTCATTCTGGTCATTTCCCCCAAAGGCATCCC
4810 4820 4830 4840 4850 4860

SEQ_ID_N1.se

AF042792.seq AGCCTGGGGGCCAGTGGGGAACTGAGGGCAAGGGGATATAGTGATGGGGCTCAGATGGAC
4870 4880 4890 4900 4910 4920

SEQ_ID_N1.se

AF042792.seq TGGGAGGAGGGGGAGGGTGATGCATTAATTAATGGCTTCGTTAATTAATGTCATGTTGCT
4930 4940 4950 4960 4970 4980

SEQ_ID_N1.se

AF042792.seq TGTCGCTTTCTCAGTGTGTGTGTGTGGTCCATGCCCACTGCTGGTGCCAGGGTGGGTGTC
4990 5000 5010 5020 5030 5040

SEQ_ID_N1.se

AF042792.seq CATGTGCACCCGGCCTGGATGCCAGCTGTGTCCTTCGGGGGCGTGCGTGTAACTGTAGTG
5050 5060 5070 5080 5090 5100

SEQ_ID_N1.se

AF042792.seq TAGTCAGGTGCTCAATGGAGAATATAAACATATACAGAAAAATATATATTTTAAGTTTAA
5110 5120 5130 5140 5150 5160

SEQ_ID_N1.se

AF042792.seq AAAACAGAAAAACAGACAAAACAATCCCCATCAGGTAGCTGTCTAACCCCCAGCTGGGTC
5170 5180 5190 5200 5210 5220

SEQ_ID_N1.se

AF042792.seq TAATCCTTCTCATTACCCACCCGACCTGGCTGCCCCTCACCTTGGGCTGGGGGACTGGGG
5230 5240 5250 5260 5270 5280

SEQ_ID_N1.se

AF042792.seq GGCCATTTCCTTTTCTCTGCCCTTTTTTTGTTGTTCTATTTTGTACAGACAAGTTGGAAA
5290 5300 5310 5320 5330 5340

SEQ_ID_N1.se

AF042792.seq AACAACAGCGACAAAAAAGTCAAGAAACTTTGTAAAATATCGTGTGTGTGATTCCTTGTA
5350 5360 5370 5380 5390 5400

SEQ_ID_N1.se

AF042792.seq AAATATTTTCAAATGGTTTATTACAGAAGATCAGTTATTAAATAATGTTCATATTTTCAC
5410 5420 5430 5440 5450 5460

SEQ_ID_N1.se

AF042792.seq TTC